

SEQUENCE LISTING



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<110> Iida, Shigeru
Tanaka, Sachiko
Inagaki, Yoshishige

<120> Genes Encoding Proteins Regulating the pH of Vacuoles

<130> 001560-397

<140> 09/830,123

<141> 2001-04-24

<150> PCT/JP00/05722

<151> 2000-08-24

<150> JP 11/236800

<151> 1999-08-24

<160> 20

<170> PatentIn version 3.1

<210> 1

<211> 2237

<212> DNA

<213> Ipomoea nil

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<221> misc_feature

<222> (1)..(2237)

<223> Nucleotide sequence of DNA encoding for protein regulating the pH of vacuoles

<400> 1

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agggattgga atgggcaacc cggatatgtg aacagaaacc acgacattgg gaaaagattt    240
attgcaaaaa ttgttttgat tgttttgat tttgtgtag aaaaagggga agaacaaaa    299
atg gcg ttc ggg ttg tct tct ttg ctc caa aat tcg gat ttg ttc acg    347
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Ser Asp His Ala Ser Val Val Ser Met Asn Leu Phe Val Ala Leu Leu
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Ile Leu Leu Leu Ser Gly Gly Lys Ser Ser His Leu Leu Val Phe Ser	
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gaa gat ctt ttc ttt ata tat ctc ctg cca cct ata ata ttc aat gcg	587
Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala	
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ggg ttt caa gtg aaa aag aag cag ttt ttc gtg aac ttc atg aca att	635
Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Val Asn Phe Met Thr Ile	
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atg ctg ttt gga gct att ggc aca ctt att agc tgt tct att ata tca	683
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Phe Gly Ala Val Lys Ile Phe Lys His Leu Asp Ile Asp Phe Leu Asp	
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Leu Phe Asn Ala Ile Gln Ser Phe Asp Met Thr Ser Phe Asp Pro Lys	
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Lys Leu Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Leu Met	
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 Val Pro Phe Val Ala Gly Ser Pro Val Glu Gln Ser Pro Arg
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Cys Ala Cys Ile Val Leu Gly His Leu Leu Glu Glu Asn Arg Trp Val
 35 40 45

Asn Glu Ser Ile Thr Ala Leu Ile Ile Gly Leu Cys Thr Gly Val Val
 50 55 60

Ile Leu Leu Leu Ser Gly Gly Lys Ser Ser His Leu Leu Val Phe Ser
 65 70 75 80

Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala
 85 90 95

Gly Phe Gln Val Lys Lys Lys Gln Phe Phe Val Asn Phe Met Thr Ile
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 Phe Gly Ala Val Lys Ile Phe Lys His Leu Asp Ile Asp Phe Leu Asp
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 Phe Gly Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser
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 Val Cys Thr Leu Gln Val Leu Ser Gln Asp Glu Thr Pro Leu Leu Tyr
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 180 185 190
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 195 200 205
 Ile Gly Leu His Phe Ile Gly Asn Phe Leu Tyr Leu Phe Leu Ser Ser
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 Thr Phe Leu Gly Val Gly Ile Gly Leu Leu Cys Ala Tyr Ile Ile Lys
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 290 295 300
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 Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Lys Phe Val Lys Asn Ser
 325 330 335
 Gln Gly Leu Ser Val Ala Val Ser Ser Ile Leu Val Gly Leu Ile Leu
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 Val Gly Arg Ala Ala Phe Val Phe Pro Leu Ser Phe Leu Ser Asn Leu
 355 360 365
 Ala Lys Lys Asn Ser Ser Asp Lys Ile Ser Phe Arg Gln Gln Ile Ile
 370 375 380
 Ile Trp Trp Ala Gly Leu Met Arg Gly Ala Val Ser Ile Ala Leu Ala
 385 390 395 400
 Tyr Asn Lys Phe Thr Thr Ser Gly His Thr Ser Leu His Glu Asn Ala
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Ile Met Ile Thr Ser Thr Val Thr Val Val Leu Phe Ser Thr Val Val
 420 425 430

Phe Gly Leu Met Thr Lys Pro Leu Ile Asn Leu Leu Leu Pro Pro His
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Lys Gln Met Pro Ser Gly His Ser Ser Met Thr Thr Ser Glu Pro Ser
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Ser Pro Lys His Phe Thr Val Pro Leu Leu Asp Asn Gln Pro Asp Ser
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Glu Ser Asp Met Ile Thr Gly Pro Glu Val Ala Arg Pro Thr Ala Leu
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Arg Met Leu Leu Arg Thr Pro Thr His Thr Val His Arg Tyr Trp Arg
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Val Pro Phe Val Ala Gly Ser Pro Val Glu Gln Ser Pro Arg
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 <223> MseI adaptor

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16

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14

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<223> Nucleotide 19 = "n" wherein "n" = any nucleotide

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<211> 29

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<211> 22

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<213> Artificial Sequence

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<223> CBSC2-linker

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 Phe Asp Phe Gly Thr Leu Leu Gly Asn Val Asp Arg Leu Ser Thr Ser
 5 10 15
 gat cat caa tca gtt gtg tcg ata aac tta ttc gtt gct ctt att tgc 453
 Asp His Gln Ser Val Val Ser Ile Asn Leu Phe Val Ala Leu Ile Cys
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 Ala Cys Ile Val Ile Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn
 35 40 45 50
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 Glu Ser Ile Thr Ala Leu Val Ile Gly Ser Cys Thr Gly Ile Val Ile
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 Phe Gln Val Lys Lys Lys Ser Phe Phe Arg Asn Phe Ser Thr Ile Met
 100 105 110
 ctc ttt ggg gca ctt ggc acc ttg ata tca ttc att att ata tca tta 741
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Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu Tyr Ser	
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180 185 190	
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Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Lys His Thr Phe	
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325 330 335	
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 405 410 415
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 His Leu Ser Arg Met Ile Ser Ser Glu Pro Thr Thr Pro Lys Ser Phe
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 Arg Pro Val Phe Gly Gly Arg Gly Phe Val Pro Phe Ala Pro Gly Ser
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<210> 15
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 Thr Ser Asp His Gln Ser Val Val Ser Ile Asn Leu Phe Val Ala Leu
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 35 40 45
 Met Asn Glu Ser Ile Thr Ala Leu Val Ile Gly Ser Cys Thr Gly Ile
 50 55 60
 Val Ile Leu Leu Ile Ser Gly Gly Lys Asn Ser His Ile Leu Val Phe
 65 70 75 80
 Ser Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn
 85 90 95
 Ala Gly Phe Gln Val Lys Lys Lys Ser Phe Phe Arg Asn Phe Ser Thr
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 Ile Met Leu Phe Gly Ala Leu Gly Thr Leu Ile Ser Phe Ile Ile Ile
 115 120 125
 Ser Leu Gly Ala Ile Gly Ile Phe Lys Lys Met Asn Ile Gly Ser Leu
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 Glu Ile Gly Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ser Ala Thr Asp
 145 150 155 160
 Ser Val Cys Thr Leu Gln Val Leu Asn Gln Asp Glu Thr Pro Leu Leu
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 Tyr Ser Leu Val Phe Gly Glu Gly Val Val Asn Asp Ala Thr Ser Val
 180 185 190

Val Leu Phe Asn Ala Ile Gln Asn Phe Asp Leu Ser His Ile Asp Thr
 195 200 205
 Gly Lys Ala Met Glu Leu Val Gly Asn Phe Leu Tyr Leu Phe Ala Ser
 210 215 220
 Ser Thr Ala Leu Gly Val Ala Ala Gly Leu Leu Ser Ala Tyr Ile Ile
 225 230 235 240
 Lys Lys Leu Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Ile
 245 250 255
 Met Ile Leu Met Ala Tyr Leu Ser Tyr Met Leu Ala Glu Leu Phe Tyr
 260 265 270
 Leu Ser Ala Ile Leu Thr Val Phe Phe Ser Gly Ile Val Met Ser His
 275 280 285
 Tyr Thr Trp His Asn Val Thr Glu Ser Ser Arg Val Thr Thr Lys His
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 Thr Phe Ala Thr Leu Ser Phe Ile Ala Glu Ile Phe Ile Phe Leu Tyr
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 Val Gly Met Asp Ala Leu Asp Ile Glu Lys Trp Lys Phe Val Ser Asp
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 Ala Tyr Asn Gln Phe Thr Arg Gly Gly His Thr Gln Leu Arg Ala Asn
 405 410 415
 Ala Ile Met Ile Thr Ser Thr Ile Thr Val Val Leu Phe Ser Thr Val
 420 425 430
 Val Phe Gly Leu Met Thr Lys Pro Leu Ile Arg Ile Leu Leu Pro Ser
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 His Lys His Leu Ser Arg Met Ile Ser Ser Glu Pro Thr Thr Pro Lys
 450 455 460
 Ser Phe Ile Val Pro Leu Leu Asp Ser Thr Gln Asp Ser Glu Ala Asp
 465 470 475 480
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 485 490 495

Thr Pro Ser His Thr Val His Tyr Tyr Trp Arg Lys Phe Asp Asn Ala
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<210> 16

<211> 2553

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<213> Nierembergia hybrida

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<222> (1)..(2553)

<223> Nucleotide sequence of DNA encoding for protein regulating the
pH of vacuoles

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tcgtcttctc aatctgcttt caaatccttt ttgtttgtga tattcgatat tattcactca 180

gtttacotta atatttcttc gcactttctg aattcgagtg ctttgaagtg tgttggattt 240

cgaaaagcgg aagaaaattc agcaaaaacg ctgttgctga atttgcagca gtttgagttt 300

ttgctaaata gctaagatct gattgaattt ttactgggtg cttataggga aattcgacgt 360

cgttttgact gcaatatattg tccgtgattc ggactttgtt gaaatattgc tatttgaaat 420

ttgaatgtaa ggttgtcata gctttgccac tcggaaatac agtcagtgag aaagaaaaaa 480

aactgtgtag tgttttttcc acaagtattt ggtgaattga ggttcttgaa atg gcg 536
Met Ala

ttt gac ttt ggg act ctg ctg gga aag atg aac aac tta aca act tct 584

Phe Asp Phe Gly Thr Leu Leu Gly Lys Met Asn Asn Leu Thr Thr Ser
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gat cat caa tca gtg gtg tcg gta aac ttg ttt gtt gca ctt att tgc 632

Asp His Gln Ser Val Val Ser Val Asn Leu Phe Val Ala Leu Ile Cys
20 25 30

gcg tgt att gtg atc ggt cat tta ttg gag gaa aac aga tgg atg aat 680

Ala Cys Ile Val Ile Gly His Leu Leu Glu Glu Asn Arg Trp Met Asn
35 40 45 50

gag tcc ata act gcc ctt gtg att ggt agt tgc act gga gtc atc att 728

Glu Ser Ile Thr Ala Leu Val Ile Gly Ser Cys Thr Gly Val Ile Ile
55 60 65

cta cta ata agt gga gga aag aac tca cat att tta gtg ttc agc gaa	776
Leu Leu Ile Ser Gly Gly Lys Asn Ser His Ile Leu Val Phe Ser Glu	
70 75 80	
gat ctt ttc ttc att tac ctt ctt cca ccg atc att ttt aat gct ggg	824
Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn Ala Gly	
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Phe Gln Val Lys Lys Lys Ser Phe Phe Arg Asn Phe Ser Thr Ile Met	
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Gly Asp Tyr Leu Ala Ile Gly Ala Ile Phe Ala Ala Thr Asp Ser Val	
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Cys Thr Leu Gln Val Leu Asn Gln Glu Glu Thr Pro Leu Leu Tyr Ser	
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Ala Leu Gln Leu Ile Gly Asn Phe Leu Tyr Leu Phe Ala Ser Ser Thr	
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Leu Tyr Phe Gly Arg His Ser Thr Asp Arg Glu Val Ala Ile Met Ile	
245 250 255	
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Gly Ile Leu Thr Val Phe Phe Cys Gly Ile Val Met Ser His Tyr Thr	
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Ala	Thr	Leu	Ser	Phe	Ile	Ala	Glu	Ile	Phe	Ile	Phe	Leu	Tyr	Val	Gly		
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Met	Asp	Ala	Leu	Asp	Ile	Glu	Lys	Trp	Lys	Phe	Val	Ser	Asp	Ser	Pro		
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Gly	Arg	Gly	Ala	Phe	Val	Phe	Pro	Leu	Ser	Phe	Leu	Ser	Asn	Leu	Thr		
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Trp	Trp	Ala	Gly	Leu	Met	Arg	Gly	Ala	Val	Ser	Met	Ala	Leu	Ala	Tyr		
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Asn	Gln	Phe	Thr	Arg	Gly	Gly	His	Thr	Gln	Leu	Arg	Ala	Asn	Ala	Ile		
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cct act gaa ccg gtc gaa ccg acc gaa cca aga cca gcc gaa tca aga 2168
Pro Thr Glu Pro Val Glu Pro Thr Glu Pro Arg Pro Ala Glu Ser Arg
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cca acc gaa cca act gat gag tgattacact gatggagatg caggttgac 2219
Pro Thr Glu Pro Thr Asp Glu
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cagatacgta atttcagctc agttcccag gtgaaccctt tagaggtttt cttcctgacg 2399
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Ile Cys Ala Cys Ile Val Ile Gly His Leu Leu Glu Glu Asn Arg Trp
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Met Asn Glu Ser Ile Thr Ala Leu Val Ile Gly Ser Cys Thr Gly Val
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Ile Ile Leu Leu Ile Ser Gly Gly Lys Asn Ser His Ile Leu Val Phe
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Ser Glu Asp Leu Phe Phe Ile Tyr Leu Leu Pro Pro Ile Ile Phe Asn
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Ala Gly Phe Gln Val Lys Lys Lys Ser Phe Phe Arg Asn Phe Ser Thr
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Ile Met Leu Phe Gly Ala Val Gly Thr Leu Ile Ser Phe Ile Ile Ile

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Ser	Val	Cys	Thr	Leu	Gln	Val	Leu	Asn	Gln	Glu	Glu	Thr	Pro	Leu	Leu	
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Lys	Lys	Leu	Tyr	Phe	Gly	Arg	His	Ser	Thr	Asp	Arg	Glu	Val	Ala	Ile	
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Leu Gly Arg His Val Pro Arg Pro His Ser Leu Arg Met Leu Leu Ser
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Thr Pro Ser His Thr Val His Tyr Tyr Trp Arg Lys Phe Asp Asn Ala
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Phe Met Arg Pro Val Phe Gly Gly Arg Gly Phe Val Pro Phe Val Pro
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Ile	Val	Ile	Gly	His	Leu	Leu	Glu	Glu	Asn	Arg	Trp	Met	Asn	Glu	Ser		
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Gln Thr Ser Gln Gly Gly Glu Pro Val Ala Arg Pro Ser Ser Leu Arg
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Leu Trp Ser Ser Gly His Gly Ser Val Val Ala Ile Thr Leu Phe Val
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 Phe Asn Ala Gly Phe Gln Val Lys Lys Lys Ser Phe Phe Arg Asn Phe
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 Ile Ile Ser Leu Gly Thr Ile Ala Phe Phe Pro Lys Met Asn Met Arg
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Asn Ala Ile Phe Ile Thr Ser Thr Ile Thr Ile Val Leu Phe Ser Thr
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Val Val Phe Gly Leu Met Thr Lys Pro Leu Ile Asn Leu Leu Ile Pro
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